

SEQUENCE LISTING

<110> BROUN, Pierre
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 SOMERVILLE, Chris

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY
 MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921
 <141> 1999-03-04

<150> 08/597,313
 <151> 1996-02-06

<150> PCT/US97/02187
 <151> 1997-02-06

<160> 15

<170> PatentIn Ver. 2.1

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 <212> DNA
 <213> Lesquerella fendleri

<400> 1

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 TC 1600 MAIL ROOM

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 <213> Lesquerella fendleri

<400> 3
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<210> 4
 <211> 384
 <212> PRT
 <213> Lesquerella fendleri

<400> 4

Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
 1 5 10 15

Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
 20 25 30

Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
 50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
 65 70 75 80

Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
 85 90 95

Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
 100 105 110

Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
 115 120 125

Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
 130 135 140

His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
 145 150 155 160

Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
 165 170 175

Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
 180 185 190

Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
 195 200 205

Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu
 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240

Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
 245 250 255

Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
 260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
 275 280 285

Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300

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Leu Asn Lys Val` Phe His Asn Ile Thr Asp Thr His Val Ala His His			
305	310	315	320
Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala			
325	330	335	
Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp			
340	345	350	
Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro			
355	360	365	
Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Asn Asn Lys Leu			
370	375	380	

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<211> 387			
<212> PRT			
<213> Ricinus communis			
 <400> 5			
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1	5	10	15
Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys			
20	25	30	
Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys			
35	40	45	
Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val			
50	55	60	
Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr			
65	70	75	80
Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe			
85	90	95	
Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly			
100	105	110	
His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu			
115	120	125	
Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser			
130	135	140	
His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val			
145	150	155	160
Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser			
165	170	175	

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
 180 185 190
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 195 200 205
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
 210 215 220
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
 225 230 235 240
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
 245 250 255
 Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
 260 265 270
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
 275 280 285
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
 290 295 300
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
 305 310 315 320
 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
 325 330 335
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
 340 345 350
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
 355 360 365
 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
 370 375 380
 Asn Lys Tyr
 385

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 <212> PRT
 <213> Arabidopsis thaliana

 <400> 6
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 Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
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 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser

35	40	45	
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser			
50	55	60	
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro			
65	70	75	80
Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val			
85	90	95	
Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe			
100	105	110	
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser			
115	120	125	
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His			
130	135	140	
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys			
145	150	155	160
Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu			
165	170	175	
Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu			
180	185	190	
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys			
195	200	205	
His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln			
210	215	220	
Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr			
225	230	235	240
Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly			
245	250	255	
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu			
260	265	270	
Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp			
275	280	285	
Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu			
290	295	300	
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu			
305	310	315	320
Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile			
325	330	335	
Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr			

340	345	350	
Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp			
355	360	365	
Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu			
370	375	380	
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<211> 384			
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<213> Brassica napus			
<220>			
<221> PEPTIDE			
<222> (1)..(384)			
<223> encodes for hydroxylane enzyme for Brassica napus			
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Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr			
20	25	30	
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser			
35	40	45	
Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser			
50	55	60	
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro			
65	70	75	80
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val			
85	90	95	
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe			
100	105	110	
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser			
115	120	125	
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His			
130	135	140	
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg			
145	150	155	160
Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Phe Gly			
165	170	175	
Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr			
180	185	190	
Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys			

195	200	205
His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln		
210	215	220
Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu		
225	230	235
Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg		
245	250	255
Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu		
260	265	270
Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp		
275	280	285
Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu		
290	295	300
Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu		
305	310	315
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile		
325	330	335
Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val		
340	345	350
Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp		
355	360	365
Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu Xaa		
370	375	380

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 <211> 309
 <212> PRT
 <213> Glycine max

<400> 8			
Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp Leu Ser Phe Ala			
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Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Gln Pro			
20	25	30	
Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu			
35	40	45	
Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val			
50	55	60	

Asp	Asp	Val	Val	Gly	Leu	Thr	Leu	His	Ser	Thr	Leu	Leu	Val	Pro	Tyr
65					70						75			80	
Phe	Ser	Trp	Lys	Ile	Ser	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser
				85							90			95	
Leu	Asp	Arg	Asp	Glu	Arg	Val	Lys	Val	Ala	Trp	Phe	Ser	Lys	Tyr	Leu
	100					105						110			
Asn	Asn	Pro	Leu	Gly	Arg	Ala	Val	Ser	Leu	Leu	Val	Thr	Leu	Thr	Ile
	115					120						125			
Gly	Trp	Pro	Met	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp
	130				135						140				
Ser	Phe	Ala	Ser	His	Tyr	His	Pro	Tyr	Arg	Val	Arg	Leu	Leu	Ile	Tyr
	145					150					155			160	
Val	Ser	Asp	Val	Ala	Leu	Phe	Ser	Val	Thr	Tyr	Ser	Leu	Tyr	Arg	Val
	165							170					175		
Ala	Thr	Leu	Lys	Gly	Leu	Val	Trp	Leu	Leu	Cys	Val	Tyr	Gly	Val	Pro
	180							185				190			
Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Thr	Ile	Thr	Tyr	Leu	Arg	Val
	195							200				205			
His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	Trp	Leu	Lys	Gly	Ala	Leu	Ala	Thr
	210					215					220				
Met	Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	His	Ile	Thr
	225					230					235			240	
Asp	Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His
	245							250					255		
Leu	Arg	Val	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Asp	Thr
	260							265					270		
Pro	Phe	Tyr	Lys	Ala	Leu	Trp	Arg	Glu	Ala	Arg	Glu	Cys	Leu	Tyr	Val
	275							280					285		
Glu	Pro	Asp	Glu	Gly	Thr	Ser	Glu	Lys	Gly	Val	Tyr	Trp	Tyr	Arg	Asn
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Lys	Tyr	Leu	Arg	Val											
	305														

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 <211> 302
 <212> PRT
 <213> Glycine max

<400> 9
 Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe Cys Leu Tyr Tyr
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Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro Leu Ser Phe Arg
 20 25 30

Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val
 35 40 45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly
 50 55 60

Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr
 65 70 75 80

Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu
 85 90 95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg
 100 105 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu
 115 120 125

Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr
 130 135 140

Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu
 145 150 155 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala
 165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe
 180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp
 195 200 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 225 230 235 240

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr
 245 250 255

Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala
 260 265 270

Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly
 275 280 285

Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val
 290 295 300

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<211> 372
<212> PRT
<213> Zea mays

<220>
<221> PEPTIDE
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<223> Desaturase

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Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro
35 40 45

His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His
50 55 60

Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile
65 70 75 80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp
85 90 95

Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val
100 105 110

Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys
115 120 125

Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp
130 135 140

Glu Val Phe Val Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro
145 150 155 160

Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln
165 170 175

Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg
180 185 190

Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr
195 200 205

Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val
210 215 220

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp
225 230 235 240

Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp
245 250 255

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His
 260 265 270
 Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met
 275 280 285
 Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
 290 295 300
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
 305 310 315 320
 Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His
 325 330 335
 Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu
 340 345 350
 Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn
 355 360 365
 Lys Lys Phe Xaa
 370

<210> 11

<211> 224

<212> PRT

<213> Ricinus communis

<400> 11

Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln
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Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val
 20 25 30

Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr
 35 40 45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser
 50 55 60

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
 65 70 75 80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe
 85 90 95

Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro
 100 105 110

Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser
 115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile

130 135 140
Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu
145 150 155 160
Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His
165 170 175
Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly
180 185 190
Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
195 200 205
His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro
210 215 220

<210> 12
<211> 20
<212> DNA
<213> Ricinus communis

<400> 12
gctctttgt gcgctcattc 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced desaturase
sequence for use as oligonucleotide primer

<400> 13
cggtaccaga aaacgccttg 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220> <223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced desaturase
sequence for use as oligonucleotide primer

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<222> (1)..(20)

<400> 14

taywsncaym gnmgnca

20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced desaturase
sequence for use as oligonucleotide primer

<400> 15

rtgrtgngcn acrtgngtrt c

21